



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/845,570  
Source: 1600  
Date Processed by STIC: 1/16/03

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
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U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002



Does Not Comply  
Corrected: Dickette Neer

~~TYPE~~  
1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/845,570

DATE: 01/16/2003

TIME: 12:31:14

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\01162003\I845570.raw

If Patent In 2.0 was  
used, see p.3

E--> 2 <100> GENERAL INFORMATION  
C--> 3 <140> CURRENT APPLICATION NUMBER: US/09/845,570  
C--> 3 <141> CURRENT FILING DATE: 2001-04-30  
W--> 0 <110> APPLICANT:  
W--> 0 <120> TITLE INVENTION: } mandatory information missing  
W--> 0 <130> FILE REFERENCE:  
E--> 3 <160> NUMBER OF SEQ ID NOS: NUMBER OF SEQ ID NOS: 5  
E--> 4 <200> SEQUENCE CHARACTERISTICS -delete! - invalid header field

## ERRORED SEQUENCES

E--> 5 <210> SEQ ID NO: (SEQ ID NO) 1  
6 <211> LENGTH: (LENGTH) 5  
E--> 7 <212> TYPE: (TYPE) [amino acid] -> change to PRT, for amino acid sequences - response can only be DNA, RNA, or PRT  
C--> 8 <213> ORGANISM: (ORGANISM) Artificial sequence  
W--> 9 <220> FEATURE:  
9 <223> OTHER INFORMATION: (Other information) YIGSR  
E--> 10 <400> SEQUENCE: (SEQUENCE) 1  
11 Tyr Ile Gly Ser Arg  
12 1 5

E--> 13 ~~<200> SEQUENCE CHARACTERISTICS~~  
E--> 14 <210> SEQ ID NO: (SEQ ID NO) 2  
15 <211> LENGTH: (LENGTH) 4  
E--> 16 <212> TYPE: (TYPE) [amino acid] -> PRT  
C--> 17 <213> ORGANISM: (ORGANISM) Artificial sequence  
W--> 18 <220> FEATURE:  
18 <223> OTHER INFORMATION: (Other information) REDV  
E--> 19 <400> SEQUENCE: (SEQUENCE) 2  
20 Arg Glu Asp Val

E--> 21 ~~<200> SEQUENCE CHARACTERISTICS~~  
E--> 22 <210> SEQ ID NO: (SEQ ID NO) 3  
23 <211> LENGTH: (LENGTH) 5  
E--> 24 <212> TYPE: (TYPE) [amino acid] -> PRT  
C--> 25 <213> ORGANISM: (ORGANISM) Artificial sequence  
W--> 26 <220> FEATURE:  
26 <223> OTHER INFORMATION: (Other information) IKVAV  
E--> 27 <400> SEQUENCE: SEQUENCE: 3  
28 Ile Lys Val Ala Val  
29 1 5

E--> 30 ~~<200> SEQUENCE CHARACTERISTICS~~  
E--> 31 <210> SEQ ID NO: (SEQ ID NO) 4  
32 <211> LENGTH: (LENGTH) 4

Each sequence begins with <210> -see Sequence Rules §1.823(b)

per Sequence Rules §1.823(b)

Delete all circled items

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Input Set : A:\SEQUENCE LISTING.txt

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E--> 33 <212> TYPE: TYPE: amino acid } change to PRT  
C--> 34 <213> ORGANISM: ORGANISM: Artificial sequence  
W--> 35 <220> FEATURE:  
35 <223> OTHER INFORMATION: Other information: KRSR  
E--> 36 <400> SEQUENCE: SEQUENCE: 4  
37 Lys Arg Ser Arg  
E--> 38 ~~<200> SEQUENCE CHARACTERISTICS~~  
E--> 39 <210> SEQ ID NO: SEQ ID NO 5  
40 <211> LENGTH: LENGTH 4  
E--> 41 <212> TYPE: TYPE: amino acid } → PRT  
C--> 42 <213> ORGANISM: ORGANISM: Artificial sequence  
W--> 43 <220> FEATURE:  
43 <223> OTHER INFORMATION: Other information: GRGD  
E--> 44 <400> SEQUENCE: SEQUENCE: 5  
45 Gly Arg Gly Asp

RAW SEQUENCE LISTING ERROR SUMMARY  
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PatentIn 2.0 "bug":

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/845,570

DATE: 01/16/2003

TIME: 12:31:15

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\01162003\I845570.raw

L:2 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
L:3 M:270 C: Current Application Number differs, Replaced Current Application No  
L:3 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:0 M:201 W: Mandatory field data missing, <110> APPLICANT NAME  
L:0 M:201 W: Mandatory field data missing, <120> TITLE INVENTION  
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE  
L:3 M:212 E: (34) Invalid or duplicate Sequence ID Number, Number Of Sequences Unknown  
L:3 M:283 W: Missing Blank Line separator, <160> field identifier  
L:4 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
L:5 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:5 M:283 W: Missing Blank Line separator, <210> field identifier  
L:7 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:8 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:0  
L:9 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:0  
L:10 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:0  
L:10 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:10 M:283 W: Missing Blank Line separator, <400> field identifier  
L:13 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
L:14 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:14 M:283 W: Missing Blank Line separator, <210> field identifier  
L:16 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:17 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:0  
L:18 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:0  
L:19 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:0  
L:19 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:19 M:283 W: Missing Blank Line separator, <400> field identifier  
L:21 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
L:22 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:22 M:283 W: Missing Blank Line separator, <210> field identifier  
L:24 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:25 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:0  
L:26 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:0  
L:27 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:0  
L:27 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:27 M:283 W: Missing Blank Line separator, <400> field identifier  
L:30 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
L:31 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:31 M:283 W: Missing Blank Line separator, <210> field identifier  
L:33 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:  
L:34 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:0  
L:35 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:0  
L:36 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:0  
L:36 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:36 M:283 W: Missing Blank Line separator, <400> field identifier  
L:38 M:250 E: Invalid Numeric Identifier, INVALID IDENTIFIER  
L:39 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:39 M:283 W: Missing Blank Line separator, <210> field identifier  
L:41 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

## VERIFICATION SUMMARY

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TIME: 12:31:15

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\01162003\I845570.raw

L:42 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:0  
L:43 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:0  
L:44 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:0  
L:44 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO  
L:44 M:283 W: Missing Blank Line separator, <400> field identifier  
L:3 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (0) Counted (5)